Supporting Information S4 for 'Modelling misclassification in multi-species acoustic data when estimating occupancy and relative activity'

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Additional simulation results

Table 1: Average ψ_1 95% PI widths for the two-species models under the different simulation scenarios (based on values of ψ_2 and λ_2). The two-species count model is described in the main text and the two-species binary detection model was developed in (Chambert et al., 2018a). We compared the relative widths of the average 95% for the analyses with binary observations to those from analyses with the call counts.

ψ_2	λ_2	Counts	Binary	Ratio (Binary/Counts)
0.25	0.5	0.165	0.177	1.069
0.25	1.0	0.167	0.175	1.047
0.25	2.0	0.148	0.156	1.057
0.25	4.0	0.141	0.144	1.020
0.50	0.5	0.176	0.194	1.106
0.50	1.0	0.188	0.204	1.088
0.50	2.0	0.169	0.183	1.084
0.50	4.0	0.159	0.167	1.045
0.75	0.5	0.179	0.205	1.141
0.75	1.0	0.201	0.228	1.138
0.75	2.0	0.197	0.215	1.092
0.75	4.0	0.190	0.202	1.062
1.00	0.5	0.175	0.207	1.180
1.00	1.0	0.202	0.246	1.214
1.00	2.0	0.235	0.291	1.241
1.00	4.0	0.262	0.320	1.220

Table 2: Average λ_1 95% PI widths for the two-species models under the different simulation scenarios (based on values of ψ_2 and λ_2). The two-species count model is described in the main text and the two-species binary detection model was developed in (Chambert et al., 2018a). We compared the relative widths of the average 95% for the analyses with binary observations to those from analyses with the call counts.

ψ_2	λ_2	Counts	Binary	Ratio (Binary/Counts)
0.25	0.5	0.344	0.447	1.301
0.25	1.0	0.350	0.446	1.274
0.25	2.0	0.328	0.418	1.273
0.25	4.0	0.303	0.389	1.286
0.50	0.5	0.376	0.503	1.340
0.50	1.0	0.411	0.540	1.314
0.50	2.0	0.384	0.510	1.328
0.50	4.0	0.352	0.466	1.323
0.75	0.5	0.391	0.533	1.366
0.75	1.0	0.457	0.634	1.388
0.75	2.0	0.454	0.643	1.417
0.75	4.0	0.436	0.620	1.423
1.00	0.5	0.397	0.575	1.448
1.00	1.0	0.454	0.685	1.508
1.00	2.0	0.528	0.846	1.604
1.00	4.0	0.625	1.034	1.656

Table 3: Coverage of ψ_1 95% PIs for the different simulation scenarios and fitted models. These results are shown in main text Figure 3 as well. Models correspond to 1: two-species, count detections (our model); 2: single-species, count detections (Chambert, Waddle, Miller, Walls, & Nichols, 2018b); 3: two-species, binary detections (Chambert et al., 2018a); and 4: single-species, binary detections (Chambert, Miller, & Nichols, 2015)

Scenario		Model			
ψ_2	λ_2	1	2	3	4
0.25	0.5	0.952	0.944	0.947	0.939
0.25	1.0	0.956	0.800	0.972	0.870
0.25	2.0	0.952	0.508	0.940	0.608
0.25	4.0	0.952	0.400	0.943	0.306
0.50	0.5	0.956	0.920	0.956	0.927
0.50	1.0	0.952	0.796	0.956	0.760
0.50	2.0	0.968	0.372	0.964	0.412
0.50	4.0	0.952	0.036	0.972	0.040
0.75	0.5	0.948	0.948	0.948	0.915
0.75	1.0	0.948	0.916	0.964	0.904
0.75	2.0	0.956	0.764	0.960	0.748
0.75	4.0	0.932	0.336	0.940	0.320
1.00	0.5	0.976	0.968	0.960	0.952
1.00	1.0	0.940	0.940	0.932	0.944
1.00	2.0	0.948	0.960	0.952	0.949
1.00	4.0	0.952	0.948	0.948	0.939

Table 4: Coverage of λ_1 95% PIs for the different simulation scenarios and fitted models. These results are shown in main text Figure 3 as well. Models correspond to 1: two-species, count detections (our model); 2: single-species, count detections (Chambert, Waddle, Miller, Walls, & Nichols, 2018b); 3: two-species, binary detections (Chambert et al., 2018a); and 4: single-species, binary detections (Chambert, Miller, & Nichols, 2015)

Scenario		Model			
ψ_2	λ_2	1	2	3	4
0.25	0.5	0.952	0.216	0.931	0.537
0.25	1.0	0.936	0.280	0.944	0.650
0.25	2.0	0.964	0.772	0.964	0.920
0.25	4.0	0.952	0.116	0.947	0.556
0.50	0.5	0.940	0.324	0.940	0.580
0.50	1.0	0.956	0.296	0.944	0.612
0.50	2.0	0.968	0.788	0.944	0.932
0.50	4.0	0.952	0.036	0.956	0.180
0.75	0.5	0.980	0.336	0.960	0.581
0.75	1.0	0.940	0.488	0.980	0.744
0.75	2.0	0.944	0.696	0.952	0.936
0.75	4.0	0.920	0.788	0.948	0.512
1.00	0.5	0.948	0.460	0.972	0.688
1.00	1.0	0.948	0.568	0.948	0.771
1.00	2.0	0.964	0.668	0.960	0.788
1.00	4.0	0.948	0.779	0.944	0.801

REFERENCES

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